



SEQUENCE LISTING

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<110> Vernet et al.

<120> Novel Polypeptides and Nucleic Acids Encoding Same

<130> 15966-672

<140> 09/783,436

<141> 2001-02-14

<150> 60/182,637

<151> 2000-02-15

<150> 60/237,862

<151> 2000-10-04

<150> 60/240,316

<151> 2000-10-13

<150> 09/783,436

<151> 2001-02-14

<160> 75

<170> PatentIn Ver. 2.1

<210> 1

<211> 579

<212> DNA

<213> Homo sapiens

<400> 1

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cccgtgaccc atgctgtgga cttcatgttc taggaggtag agggagacag acaagaatca 480
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<211> 94

<212> PRT

<213> Homo sapiens

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      20           25           30
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Thr Ala Lys Ser Glu Asp Ser Gly Trp Cys Gly Pro Val Cys Lys Glu
35 40 45

Ser Ser Gly His Gly Ile Arg Pro Leu His Ser Ser Arg Ser Phe Asn
50 55 60

Pro Ile Ser Thr His Thr Ser Leu Cys Ala Leu Thr Pro Pro Gln Pro
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Phe Trp Asn Lys Thr Ile Thr Ala Gln Gly Leu Gln Asp Val
85 90

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<211> 692
<212> DNA
<213> Homo sapiens

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gatccacctc tataagttgc aggttgagta tctcttatct gaaatgctag agaccagaag 240
tgtttcaggt ttcagatatt tagattttgg aatatttgca tatacacgag atatccaggg 300
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tagcctgaag gtaattttat acagtattta taatttgtcc aaggaacaaa gttttgactg 420
tgttttgact atgactcgtc atgtgaagtc atatgtggaa ttttccactt gtggcatcac 480
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ccgggcagcc gctcgagccc tatagttagt aa 692

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<211> 115
<212> PRT
<213> Homo sapiens

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Ile Phe Ala Tyr Thr Arg Asp Ile Gln Gly Lys Arg Pro Lys Ser Lys
20 25 30

His Glu Ile His Leu Cys Phe Ile Tyr Thr Ser Tyr Ile Tyr Ser Leu
35 40 45

Lys Val Ile Leu Tyr Ser Ile Tyr Asn Leu Ser Lys Glu Gln Ser Phe
50 55 60

Asp Cys Val Leu Thr Met Thr Arg His Val Lys Ser Tyr Val Glu Phe
65 70 75 80

Ser Thr Cys Gly Ile Thr Gln Ala Leu Lys Lys Leu Gln Ile Trp Glu
85 90 95

His Ile Gly Phe Arg Ile Phe Arg Leu Gly Met Leu Asn Pro Tyr Ser
 100 105 110

Val Tyr Gln
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<210> 5
 <211> 2351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (408)
 <223> Where n is an A, T, G, or C

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 cgccactgca ctccagcctg ggcgacagag cgagactccg tctcaaaaaa aaaaaaaaaaag 180
 aacatcctga gccgggctg gaaaagctct ttgcagatgg cgcttccatc tctgcgcccc 240
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tcataattaa a

2351

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<211> 617

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (50)

<223> Wherein Xaa is any amino acid as disclosed in the
specification

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Asn Ile Leu Glu Thr Leu Phe His Thr Trp Met Val Pro Ala Ile Asp
35 40 45

Pro Xaa Val Ser Phe Tyr His Ala Asp Gln Leu Lys Pro Gln Val Ser
50 55 60

Trp Ile Pro Asn Lys His Tyr Ser Gly Leu Tyr Gly Leu Met Lys Leu
65 70 75 80

Val Leu Pro Asn Ala Leu Pro Ala Glu Leu Ala Arg Val Ile Val Leu
85 90 95

Asp Thr Asp Val Thr Phe Ala Ser Asp Ile Ser Glu Leu Trp Ala Leu
100 105 110

Phe Ala His Phe Ser Asp Thr Gln Ala Ile Gly Leu Val Glu Asn Gln
115 120 125

Ser Asp Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro
130 135 140

Ala Leu Gly Arg Gly Phe Asn Thr Gly Val Ile Leu Leu Arg Leu Asp
145 150 155 160

Arg Leu Arg Gln Ala Gly Trp Glu Gln Met Trp Arg Leu Thr Ala Arg
165 170 175

Arg Glu Leu Leu Ser Leu Pro Ala Thr Ser Leu Ala Asp Gln Asp Ile
180 185 190

Phe Asn Ala Val Ile Lys Glu His Pro Gly Leu Val Gln Arg Leu Pro
195 200 205

Cys Val Trp Asn Val Gln Leu Ser Asp His Thr Leu Ala Glu Arg Cys
210 215 220

Tyr Ser Glu Ala Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys
225 230 235 240
Lys Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Phe Tyr
245 250 255
Leu Thr Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe
260 265 270
Val Cys Pro Ser Gln Pro Pro Pro Gly Ala Glu Gln Leu Gln Gln Ala
275 280 285
Leu Ala Gln Leu Asp Glu Glu Asp Pro Cys Phe Glu Phe Arg Gln Gln
290 295 300
Gln Leu Thr Val His Arg Val His Val Thr Phe Leu Pro His Glu Pro
305 310 315 320
Pro Pro Pro Arg Pro His Asp Val Thr Leu Val Ala Gln Leu Ser Met
325 330 335
Asp Arg Leu Gln Met Leu Glu Ala Leu Cys Arg His Trp Pro Gly Pro
340 345 350
Met Ser Leu Ala Leu Tyr Leu Thr Asp Ala Glu Ala Gln Gln Phe Leu
355 360 365
His Phe Val Glu Ala Ser Pro Val Leu Ala Ala Arg Gln Asp Val Ala
370 375 380
Tyr His Val Val Tyr Arg Glu Gly Pro Leu Tyr Pro Val Asn Gln Leu
385 390 395 400
Arg Asn Val Ala Leu Ala Gln Ala Leu Thr Pro Tyr Val Phe Leu Ser
405 410 415
Asp Ile Asp Phe Leu Pro Ala Tyr Ser Leu Tyr Asp Tyr Leu Arg Ala
420 425 430
Ser Ile Glu Gln Leu Gly Leu Gly Ser Arg Arg Lys Ala Ala Leu Val
435 440 445
Val Pro Ala Phe Glu Thr Leu Arg Tyr Arg Phe Ser Phe Pro His Ser
450 455 460
Lys Val Glu Leu Leu Ala Leu Leu Asp Ala Gly Thr Leu Tyr Thr Phe
465 470 475 480
Arg Tyr His Glu Trp Pro Arg Gly His Ala Pro Thr Asp Tyr Ala Arg
485 490 495
Trp Arg Glu Ala Gln Ala Pro Tyr Arg Val Gln Trp Ala Ala Asn Tyr
500 505 510
Glu Pro Tyr Val Val Val Pro Arg Asp Cys Pro Arg Tyr Asp Pro Arg
515 520 525

Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Val Glu Leu Asp
 530 535 540
 Ala Gln Glu Tyr Glu Leu Leu Val Leu Pro Glu Ala Phe Thr Ile His
 545 550 555 560
 Leu Pro His Ala Pro Ser Leu Asp Ile Ser Arg Phe Arg Ser Ser Pro
 565 570 575
 Thr Tyr Arg Asp Cys Leu Gln Ala Leu Lys Asp Glu Phe His Gln Asp
 580 585 590
 Leu Ser Arg His His Gly Ala Ala Ala Leu Lys Tyr Leu Pro Ala Leu
 595 600 605
 Gln Gln Pro Gln Ser Pro Ala Arg Gly
 610 615

<210> 7
 <211> 812
 <212> DNA
 <213> Homo sapiens

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 gcgagggtg tagtgagcca agattgtgcc actgcactcc agcctgggca acaaagttag 180
 actcttatct tacaagaaaa aaaagaatgc ttaggaatca actcccctcc taatgcccag 240
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 agagcagggtg gcacagtaat aaatggcatc ccccgagtc cagcagggct tgttacaagt 420
 cagcttgaag agcgaccagt tattctcatt gaagtggagc tcctttttct ggccgcccag 480
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 ccctttgcac tggaggccag ggctcccgca gccgcctctg ttgcccgcga gccctgctgc 720
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 ggatggtggc ggttcccggg gctcaccgaa ta 812

<210> 8
 <211> 132
 <212> PRT
 <213> Homo sapiens

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 His Ser Arg Met Gln Gly Gly Ser Gly Thr Tyr Phe His Ser Ile Gly
 20 25 30
 Ala Ala Gly Val Leu Arg Ala Gly Gly Thr Val Ile Asn Gly Ile Pro
 35 40 45
 Arg Val Thr Ala Gly Leu Val Thr Ser Gln Leu Glu Glu Arg Pro Val

50 55 60
 Ile Leu Ile Glu Val Glu Leu Leu Phe Leu Ala Ala His Glu Glu Val
 65 70 75 80
 Leu Thr Phe Gly Tyr Lys Ala Gly Gln Gly Leu Gly Val Glu Ser Pro
 85 90 95
 Gln Leu Gly Ile Gly Ala Leu Leu Ala Ala Asp Val Ala Gln Glu Thr
 100 105 110
 Val Gln Leu Lys Leu Gly Ala Pro Gly Gly Gly Leu Thr Gly His Ala
 115 120 125
 Gln Leu Gly Gly
 130

<210> 9
 <211> 2059
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)
 <223> Where n is an A, T, G, or C

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<210> 10
 <211> 320
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro
 50 55 60
 Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val
 65 70 75 80
 Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His
 85 90 95
 Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu Ile
 100 105 110
 Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser Ala
 115 120 125
 Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe
 130 135 140
 Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg
 145 150 155 160
 Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly
 165 170 175
 Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile
 180 185 190
 Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe
 195 200 205
 Cys Phe Gln Thr Lys Val Arg Ala Trp Arg Ala Leu Pro Trp Pro Pro
 210 215 220

Asp Ser Pro Phe Leu Ser Gly Pro Asp Pro Gly Thr Leu Gly Met Phe
 225 230 235 240
 Pro Arg Asp Leu Ile Pro Phe Ser Ser Ser Ala Pro Thr Lys Leu Cys
 245 250 255
 Pro Val Ser Val Leu Arg Met Leu Trp Thr Phe Pro Tyr Pro Leu Gly
 260 265 270
 Gly Ser Thr Gly Thr Pro Trp Gln Gly Gln Ser Asp Trp Ala Gly Cys
 275 280 285
 His Ser His Leu Thr Gly Ala Ser Phe Leu Leu Pro Gly Arg Trp Thr
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 Ser Pro Arg Ala Gln Ala Ser Ser Val Ser Trp Glu Leu Cys Ser Trp
 305 310 315 320

<210> 11
 <211> 807
 <212> DNA
 <213> Homo sapiens

<400> 11
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 gaaatagaat agaaaatatc caaaaaa 807

<210> 12
 <211> 135
 <212> PRT
 <213> Homo sapiens

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 Tyr Ala Asp Pro Val Ala Asp Leu Leu Asp Lys Trp Gly Ala Phe Arg
 20 25 30
 Ala Arg Leu Phe Arg Glu Ser Cys Val Phe His Arg Gly Asn Tyr Val

35

40

45

Lys Asp Leu Ser Arg Leu Gly Arg Asp Leu Arg Arg Val Leu Ile Leu
50 55 60

Asp Asn Ser Pro Ala Ser Tyr Val Phe His Pro Asp Asn Ala Val Ser
65 70 75 80

Ala Gly Trp Thr Gly Thr Gly Thr Gly Ala Glu Thr Gln Glu Gly Val
85 90 95

Ser Pro Phe Arg Pro Pro Trp Pro Leu Gly Ser Pro Val Gly Gly Trp
100 105 110

Val Pro Ser Gln Ser Phe Leu His Ser Leu Pro Val Pro Ala Ala His
115 120 125

Ser Pro His Pro Pro Ala Leu
130 135

<210> 13

<211> 2357

<212> DNA

<213> Homo sapiens

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ctccgactgc ggcccgcagc cgccgcccgc cgcccaagtgc cgagctcttg catgtggcca 240
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tggagacgct cttccacaca tggatggtgc ctgctgtccg tgtcagcttt tatcatgccg 420
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<210> 14
 <211> 695
 <212> PRT
 <213> Homo sapiens

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      20              25              30

Arg Glu Ala Ala Glu Ser Arg Arg Pro Arg Arg Asn Pro Gly Gly Pro
      35              40              45

Ala Pro Gly Thr Thr Thr Ala Pro Thr Ala Ala Arg Ser Arg Arg Arg
      50              55              60

Pro Pro Lys Cys Glu Leu Leu His Val Ala Ile Val Cys Ala Gly His
      65              70              75              80

Asn Ser Ser Arg Asp Val Ile Ile Leu Val Lys Ser Met Leu Phe Tyr
      85              90              95

Arg Lys Asn Pro Leu His Leu His Leu Val Thr Asp Ala Val Ala Arg
      100             105             110

Asn Ile Leu Glu Thr Leu Phe His Thr Trp Met Val Pro Ala Val Arg
      115             120             125

Val Ser Phe Tyr His Ala Asp Gln Leu Lys Pro Gln Val Ser Trp Ile
      130             135             140

Pro Asn Lys His Tyr Ser Gly Leu Tyr Gly Leu Met Lys Leu Val Leu
      145             150             155             160

Pro Ser Ala Leu Pro Ala Glu Leu Ala Arg Val Ile Val Leu Asp Thr
      165             170             175

Asp Val Thr Phe Ala Ser Asp Ile Ser Glu Leu Trp Ala Leu Phe Ala
      180             185             190

His Phe Ser Asp Thr Gln Ala Ile Gly Leu Val Glu Asn Gln Ser Asp
      195             200             205

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Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro Ala Leu
 210 215 220
 Gly Arg Gly Phe Asn Thr Gly Val Ile Leu Leu Arg Leu Asp Arg Leu
 225 230 235 240
 Arg Gln Ala Gly Trp Glu Gln Met Trp Arg Leu Thr Ala Arg Arg Glu
 245 250 255
 Leu Leu Ser Leu Pro Ala Thr Ser Leu Ala Asp Gln Asp Ile Phe Asn
 260 265 270
 Ala Val Ile Lys Glu His Pro Gly Leu Val Gln Arg Leu Pro Cys Val
 275 280 285
 Trp Asn Val Gln Leu Ser Asp His Thr Leu Ala Glu Arg Cys Tyr Ser
 290 295 300
 Glu Ala Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys Lys Leu
 305 310 315 320
 Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Phe Tyr Leu Thr
 325 330 335
 Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe Val Cys
 340 345 350
 Pro Ser Gln Pro Pro Pro Gly Ala Glu Gln Leu Gln Gln Ala Leu Ala
 355 360 365
 Gln Leu Asp Glu Glu Asp Pro Cys Phe Glu Phe Arg Gln Gln Gln Leu
 370 375 380
 Thr Val His Arg Val His Val Thr Phe Leu Pro His Glu Pro Pro Pro
 385 390 395 400
 Pro Arg Pro His Asp Val Thr Leu Val Ala Gln Leu Ser Met Asp Arg
 405 410 415
 Leu Gln Met Leu Glu Ala Leu Cys Arg His Trp Pro Gly Pro Met Ser
 420 425 430
 Leu Ala Leu Tyr Leu Thr Asp Ala Glu Ala Gln Gln Phe Leu His Phe
 435 440 445
 Val Glu Ala Ser Pro Val Leu Ala Ala Arg Gln Asp Val Ala Tyr His
 450 455 460
 Val Val Tyr Arg Glu Gly Pro Leu Tyr Pro Val Asn Gln Leu Arg Asn
 465 470 475 480
 Val Ala Leu Ala Gln Ala Leu Thr Pro Tyr Val Phe Leu Ser Asp Ile
 485 490 495
 Asp Phe Leu Pro Ala Tyr Ser Leu Tyr Asp Tyr Leu Arg Ala Ser Ile
 500 505 510

Glu Gln Leu Gly Leu Gly Ser Arg Arg Lys Ala Ala Leu Val Val Pro
 515 520 525
 Ala Phe Glu Thr Leu Arg Tyr Arg Phe Ser Phe Pro His Ser Lys Val
 530 535 540
 Glu Leu Leu Ala Leu Leu Asp Ala Gly Thr Leu Tyr Thr Phe Arg Tyr
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 His Glu Trp Pro Arg Gly His Ala Pro Thr Asp Tyr Ala Arg Trp Arg
 565 570 575
 Glu Ala Gln Ala Pro Tyr Arg Val Gln Trp Ala Ala Asn Tyr Glu Pro
 580 585 590
 Tyr Val Val Val Pro Arg Asp Cys Pro Arg Tyr Asp Pro Arg Phe Val
 595 600 605
 Gly Phe Gly Trp Asn Lys Val Ala His Ile Val Glu Leu Asp Ala Gln
 610 615 620
 Glu Tyr Glu Leu Leu Val Leu Pro Glu Ala Phe Thr Ile His Leu Pro
 625 630 635 640
 His Ala Pro Ser Leu Asp Ile Ser Arg Phe Arg Ser Ser Pro Thr Tyr
 645 650 655
 Arg Asp Cys Leu Gln Ala Leu Lys Asp Glu Phe His Gln Asp Leu Ser
 660 665 670
 Arg His His Gly Ala Ala Ala Leu Lys Tyr Leu Pro Ala Leu Gln Gln
 675 680 685
 Pro Gln Ser Pro Ala Arg Gly
 690 695

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 <212> DNA
 <213> Homo sapiens

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 ctctttgtgc tctcacaccc ccacagccct tctggaataa gaccatcaca gcacagggtt 300
 tgcaagatgt ctaatgccag tcattcacag ggcagctcag accctggcct gcggtgcata 360
 ctagggtgact ccacatgagg tgtcatgcta gatcctgcag ggagaataag cacacacagg 420
 cccgtgaccc atgctgtgga cttcatgttc taggaggtag agggagacag acaagaatca 480
 aatgactgta ctaggccggg cgcactggct cagcctgta atcccagcac tttggggagg 540
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<400> 16
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<210> 17
<211> 656
<212> DNA
<213> Homo sapiens

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ctataaaaca agaaaacctc tacgtacaga tcttttaaaa ttaaagcagg catctttgct 180
gatccacctc tataagttgc aggttgagta tctcttatct gaaatgctag agaccagaag 240
tgtttcagggt ttcagatatt tagattttgg aatatttgca tatacacgag atatccaggg 300
gaagagaccc aagtctaaac atgaaattca tttatgtttc atatacacct catatatata 360
tagcctgaag gtaattttat acagtattta taatttgtcc aaggaacaaa gttttgactg 420
tgttttgact atgactcgtc atgtgaagtc atatgtggaa ttttccactt gtggcatcac 480
acaggcactc aaaaagcttc agatttgagg gcatattgga tttcgcatat tcagattagg 540
gatgctcaac ccatactcag tttaccagta aaaaaacata atgtttgcaa ttactcctcc 600
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<212> DNA
<213> Homo sapiens

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aggctgaggg aggagaatgg cgtgaacccg ggaggcagag cttgcagtga gccgagatcc 120
cgccactgca ctccagcctg ggcgacagag cgagactccg tctc 164

<210> 20

<400> 20
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<210> 21
<211> 164
<212> DNA
<213> Homo sapiens

<400> 21
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<210> 22

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<210> 23

<211> 454

<212> PRT

<213> Homo sapiens

<400> 23

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Ala Asp Glu Leu Lys Ser Glu Val Ser Trp Ile Pro Asn Lys His Tyr
35 40 45

Ser Gly Ile Tyr Gly Leu Met Lys Leu Val Leu Thr Lys Thr Leu Pro
50 55 60

Ala Asn Leu Glu Arg Val Ile Val Leu Asp Thr Asp Ile Thr Phe Ala
65 70 75 80

Thr Asp Ile Ala Glu Leu Trp Ala Val Phe His Lys Phe Lys Gly Gln
85 90 95

Gln Val Leu Gly Leu Val Glu Asn Gln Ser Asp Trp Tyr Leu Gly Asn
100 105 110

Leu Trp Lys Asn His Arg Pro Trp Pro Ala Leu Gly Arg Gly Tyr Asn
115 120 125

Thr Gly Val Ile Leu Leu Leu Leu Asp Lys Leu Arg Lys Met Lys Trp
130 135 140

Glu Gln Met Trp Arg Leu Thr Ala Glu Arg Glu Leu Met Gly Met Leu
145 150 155 160

Ser Thr Ser Leu Ala Asp Gln Asp Ile Phe Asn Ala Val Ile Lys Gln
165 170 175

Asn Pro Phe Leu Val Tyr Gln Leu Pro Cys Phe Trp Asn Val Gln Leu
180 185 190

Ser Asp His Thr Arg Ser Glu Gln Cys Tyr Arg Asp Val Ser Asp Leu
195 200 205

Lys Val Ile His Trp Asn Ser Pro Lys Lys Leu Arg Val Lys Asn Lys
210 215 220

His Val Glu Phe Phe Arg Asn Leu Tyr Leu Thr Phe Leu Glu Tyr Asp
225 230 235 240

Gly Asn Leu Leu Arg Arg Glu Leu Phe Gly Cys Pro Ser Glu Thr Asp
245 250 255

Val Asn Asn Glu Asn Leu Gln Lys Gln Leu Ser Glu Leu Asp Glu Asp
 260 265 270
 Asp Leu Cys Tyr Glu Phe Arg Arg Glu Arg Phe Thr Val His Arg Thr
 275 280 285
 His Leu Tyr Phe Leu His Tyr Glu Phe Glu Pro Ser Ala Asp Asn Thr
 290 295 300
 Asp Val Thr Leu Val Ala Gln Leu Ser Met Asp Arg Leu Gln Met Leu
 305 310 315 320
 Glu Ala Ile Cys Lys His Trp Glu Gly Pro Ile Ser Leu Ala Leu Tyr
 325 330 335
 Leu Ser Asp Ala Glu Ala Gln Gln Phe Leu Arg Tyr Ala Gln Gly Ser
 340 345 350
 Glu Val Leu Met Ser Arg Gln Asn Val Gly Tyr His Ile Val Tyr Lys
 355 360 365
 Glu Gly Gln Phe Tyr Pro Val Asn Leu Leu Arg Asn Val Ala Met Lys
 370 375 380
 His Ile Ser Thr Pro Tyr Met Phe Leu Ser Asp Ile Asp Phe Leu Pro
 385 390 395 400
 Met Tyr Gly Leu Tyr Glu Tyr Leu Arg Lys Ser Val Ile Gln Leu Asp
 405 410 415
 Leu Ala Asn Thr Lys Lys Ala Met Ile Val Pro Ala Phe Glu Thr Leu
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 Arg Tyr Arg Leu Ser Phe Pro Lys Ser Lys Ala Glu Leu Leu Ser Met
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 Leu Asp Met Gly Thr Leu
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<210> 24

<400> 24
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<210> 25
 <211> 584
 <212> PRT
 <213> Homo sapiens

<400> 25
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 20 25 30

Ala Asp Glu Leu Lys Ser Glu Val Ser Trp Ile Pro Asn Lys His Tyr
 35 40 45
 Ser Gly Ile Tyr Gly Leu Met Lys Leu Val Leu Thr Lys Thr Leu Pro
 50 55 60
 Ala Asn Leu Glu Arg Val Ile Val Leu Asp Thr Asp Ile Thr Phe Ala
 65 70 75 80
 Thr Asp Ile Ala Glu Leu Trp Ala Val Phe His Lys Phe Lys Gly Gln
 85 90 95
 Gln Val Leu Gly Leu Val Glu Asn Gln Ser Asp Trp Tyr Leu Gly Asn
 100 105 110
 Leu Trp Lys Asn His Arg Pro Trp Pro Ala Leu Gly Arg Gly Tyr Asn
 115 120 125
 Thr Gly Val Ile Leu Leu Leu Leu Asp Lys Leu Arg Lys Met Lys Trp
 130 135 140
 Glu Gln Met Trp Arg Leu Thr Ala Glu Arg Glu Leu Met Gly Met Leu
 145 150 155 160
 Ser Thr Ser Leu Ala Asp Gln Asp Ile Phe Asn Ala Val Ile Lys Gln
 165 170 175
 Asn Pro Phe Leu Val Tyr Gln Leu Pro Cys Phe Trp Asn Val Gln Leu
 180 185 190
 Ser Asp His Thr Arg Ser Glu Gln Cys Tyr Arg Asp Val Ser Asp Leu
 195 200 205
 Lys Val Ile His Trp Asn Ser Pro Lys Lys Leu Arg Val Lys Asn Lys
 210 215 220
 His Val Glu Phe Phe Arg Asn Leu Tyr Leu Thr Phe Leu Glu Tyr Asp
 225 230 235 240
 Gly Asn Leu Leu Arg Arg Glu Leu Phe Gly Cys Pro Ser Glu Ala Asp
 245 250 255
 Val Asn Ser Glu Asn Leu Gln Lys Gln Leu Ser Glu Leu Asp Glu Asp
 260 265 270
 Asp Leu Cys Tyr Glu Phe Arg Arg Glu Arg Phe Thr Val His Arg Thr
 275 280 285
 His Leu Tyr Phe Leu His Tyr Glu Tyr Glu Pro Ala Ala Asp Ser Thr
 290 295 300
 Asp Val Thr Leu Val Ala Gln Leu Ser Met Asp Arg Leu Gln Met Leu
 305 310 315 320
 Glu Ala Ile Cys Lys His Trp Glu Gly Pro Ile Ser Leu Ala Leu Tyr
 325 330 335

Leu Ser Asp Ala Glu Ala Gln Gln Phe Leu Arg Tyr Ala Gln Gly Ser
 340 345 350
 Glu Val Leu Met Ser Arg His Asn Val Gly Tyr His Ile Val Tyr Lys
 355 360 365
 Glu Gly Gln Phe Tyr Pro Val Asn Leu Leu Arg Asn Val Ala Met Lys
 370 375 380
 His Ile Ser Thr Pro Tyr Met Phe Leu Ser Asp Ile Asp Phe Leu Pro
 385 390 395 400
 Met Tyr Gly Leu Tyr Glu Tyr Leu Arg Lys Ser Val Ile Gln Leu Asp
 405 410 415
 Leu Ala Asn Thr Lys Lys Ala Met Ile Val Pro Ala Phe Glu Thr Leu
 420 425 430
 Arg Tyr Arg Leu Ser Phe Pro Lys Ser Lys Ala Glu Leu Leu Ser Met
 435 440 445
 Leu Asp Met Gly Thr Leu Phe Thr Phe Arg Tyr His Val Trp Thr Lys
 450 455 460
 Gly His Ala Pro Thr Asn Phe Ala Lys Trp Arg Thr Ala Thr Thr Pro
 465 470 475 480
 Tyr Arg Val Glu Trp Glu Ala Asp Phe Glu Pro Tyr Val Val Val Arg
 485 490 495
 Arg Asp Cys Pro Glu Tyr Asp Arg Arg Phe Val Gly Phe Gly Trp Asn
 500 505 510
 Lys Val Ala His Ile Met Glu Leu Asp Val Gln Glu Tyr Glu Phe Ile
 515 520 525
 Val Leu Pro Asn Ala Tyr Met Ile His Met Pro His Ala Pro Ser Phe
 530 535 540
 Asp Ile Thr Lys Phe Arg Ser Asn Lys Gln Tyr Arg Ile Cys Leu Lys
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<210> 26

<211> 189

<212> PRT

<213> Homo sapiens

<400> 26

Leu Ser Glu Leu Asp Glu Asp Asp Leu Cys Tyr Glu Phe Arg Arg Glu

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Glu Pro Ala Ala Asp Ser Thr Asp Val Thr Leu Val Ala Gln Leu Ser	35	40	45
Met Asp Arg Leu Gln Met Leu Glu Ala Ile Cys Lys His Trp Glu Gly	50	55	60
Pro Ile Ser Leu Ala Leu Tyr Leu Ser Asp Ala Glu Ala Gln Gln Phe	65	70	75
Leu Arg Tyr Ala Gln Gly Ser Glu Val Leu Met Ser Arg His Asn Val	85	90	95
Gly Tyr His Ile Val Tyr Lys Glu Gly Gln Phe Tyr Pro Val Asn Leu	100	105	110
Leu Arg Asn Val Ala Met Lys His Ile Ser Thr Pro Tyr Met Phe Leu	115	120	125
Ser Asp Ile Asp Phe Leu Pro Met Tyr Gly Leu Tyr Glu Tyr Leu Arg	130	135	140
Lys Ser Val Ile Gln Leu Asp Leu Ala Asn Thr Lys Lys Ala Met Ile	145	150	155
Val Pro Ala Phe Glu Thr Leu Arg Tyr Arg Leu Ser Phe Pro Lys Ser	165	170	175
Lys Ala Glu Leu Leu Ser Met Leu Asp Met Gly Thr Leu	180	185	

<210> 27

<400> 27
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<210> 28

<400> 28
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<210> 29

<211> 173

<212> DNA

<213> Homo sapiens

<400> 29

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<210> 30

<400> 30
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<210> 31
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<212> DNA
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<210> 33
<211> 1006
<212> DNA
<213> Homo sapiens

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<210> 35
<211> 928
<212> DNA
<213> Homo sapiens

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<210> 36

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<210> 37
<211> 1006
<212> DNA
<213> Homo sapiens

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<210> 38
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 38
 Leu Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu
 1 5 10 15
 Tyr Ala Ala Leu Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp
 20 25 30
 Thr Gln Leu Val Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu Asp
 35 40 45
 Tyr Ile Thr Gly Ala Leu Gln Ile Tyr Thr Asp Ile Ile Tyr Ile Phe
 50 55 60
 Thr Phe Val Leu Gln Leu Met Gly
 65 70

<210> 39
 <211> 72
 <212> PRT
 <213> Rattus rattus

<400> 39
 Leu Ala Ile Leu Leu Pro Phe Gln Tyr Val Pro Trp Leu His Ala Val
 1 5 10 15
 Tyr Ala Val Leu Gly Ala Gly Val Phe Thr Leu Phe Leu Ala Phe Asp
 20 25 30
 Thr Gln Leu Leu Met Gly Asn Arg Arg His Ser Leu Ser Pro Glu Glu
 35 40 45
 Tyr Ile Phe Gly Ala Leu Asn Ile Tyr Leu Asp Ile Ile Tyr Ile Phe
 50 55 60
 Thr Phe Phe Leu Gln Leu Phe Gly
 65 70

<210> 40

<400> 40
 000

<210> 41
 <211> 549
 <212> DNA
 <213> Homo sapiens

<400> 41
 agtacgcaga cccagtagct gacctgctgg acaaattgggg ggccttccgg gcccggtgt 60
 ttcgagagtc ctgcgtcttc caccggggga actacgtgaa ggacctgagc cggttgggtc 120

gagacctgcg gcgggtgctc atcctggaca attcacctgc ctccctatgtc ttccatccag 180
acaatgctgt gagtgcgggc tggactggga ctgggacagg agctgagacc caggaagggg 240
tcagtccatt caggccacct tggcctcttg gatccccagt tgggggggtgg gtgccctccc 300
agtccttcct gcattcattg cctgtgcctg ccgcccactc ccctcatcca cctgccctgt 360
agccatatgg tcttttcccc tcgcacaaag cagagcatct gccatgcaca ggggccccca 420
cagggcaacg gagtttggaa agtttcaatt tttcgaattg ccagttgtga cctactgatg 480
gcccacagaa ttaatttagt gggttctgat tgggaatttt aacaaaatga aatagaatag 540
aaaatatcc 549

<210> 42
<211> 549
<212> DNA
<213> Homo sapiens

<400> 42
agtacgcaga cccagtagct gacctgctgg acaaatgggg ggccttccgg gcccggtgt 60
ttcgagagtc ctgcgtcttc caccggggga actacgtgaa ggacctgagc cggttgggtc 120
gagacctgcg gcgggtgctc atcctggaca attcacctgc ctccctatgtc ttccatccag 180
acaatgctgt gagtgcgggc tggactggga ctgggacagg agctgagacc caggaagggg 240
tcagtccatt caggccacct tggcctcttg gatccccagt tgggggggtgg gtgccctccc 300
agtccttcct gcattcattg cctgtgcctg ccgcccactc ccctcatcca cctgccctgt 360
agccatatgg tcttttcccc tcgcacaaag cagagcatct gccatgcaca ggggccccca 420
cagggcaacg gagtttggaa agtttcaatt tttcgaattg ccagttgtga cctactgatg 480
gcccacagaa ttaatttagt gggttctgat tgggaatttt aacaaaatga aatagaatag 540
aaaatatcc 549

<210> 43

<400> 43
000

<210> 44
<211> 376
<212> DNA
<213> Homo sapiens

<400> 44
tcgacctgga cgagaccctg gtgcacagct ctttcaagcc agtgaacaac gcggacttca 60
tcatccctgt ggagattgat ggggtgggtcc accaggtcta cgtgttgaag cgtcctcacg 120
tggatgagtt cctgcagcga atgggcgagc tctttgaatg tgtgctgttc actgctagcc 180
tcgccaagta cgcagaccca gtagctgacc tgctggacaa atggggggcc ttccggggccc 240
ggctgttttc agagtcctgc gtcttccacc gggggaacta cgtgaaggac ctgagccggt 300
tgggtcgaga cctgcggcgg gtgctcatcc tggacaattc acctgcctcc tatgtcttcc 360
atccagacaa tgctgt 376

<210> 45

<400> 45
000

<210> 46
<211> 157
<212> DNA

<213> Homo sapiens

<400> 46

tctggaatgt gcagctgtca gaccacaccc gctccgagca gtgctacaga gacgtgtctg 60
atctaaaggt cattcactgg aactccccca agaagctccg ggtgaagaac aagcatgtgg 120
agttttttcg caacctctac ctgaccttcc tggagta 157

<210> 47

<400> 47

000

<210> 48

<211> 619

<212> PRT

<213> Homo sapiens

<400> 48

Lys Cys Glu Thr Ile His Val Ala Ile Val Cys Ala Gly Tyr Asn Ala
1 5 10 15

Ser Arg Asp Val Val Thr Leu Val Lys Ser Val Leu Phe His Arg Arg
20 25 30

Asn Pro Leu His Phe His Leu Ile Ala Asp Ser Ile Ala Glu Gln Ile
35 40 45

Leu Ala Thr Leu Phe Gln Thr Trp Met Val Pro Ala Val Arg Val Asp
50 55 60

Phe Tyr Asn Ala Asp Glu Leu Lys Ser Glu Val Ser Trp Ile Pro Asn
65 70 75 80

Lys His Tyr Ser Gly Ile Tyr Gly Leu Met Lys Leu Val Leu Thr Lys
85 90 95

Thr Leu Pro Ala Asn Leu Glu Arg Val Ile Val Leu Asp Thr Asp Ile
100 105 110

Thr Phe Ala Thr Asp Ile Ala Glu Leu Trp Ala Val Phe His Lys Phe
115 120 125

Lys Gly Gln Gln Val Leu Gly Leu Val Glu Asn Gln Ser Asp Trp Tyr
130 135 140

Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro Ala Leu Gly Arg
145 150 155 160

Gly Tyr Asn Thr Gly Val Ile Leu Leu Leu Leu Asp Lys Leu Arg Lys
165 170 175

Met Lys Trp Glu Gln Met Trp Arg Leu Thr Ala Glu Arg Glu Leu Met
180 185 190

Gly Met Leu Ser Thr Ser Leu Ala Asp Gln Asp Ile Phe Asn Ala Val
195 200 205

Ile Lys Gln Asn Pro Phe Leu Val Tyr Gln Leu Pro Cys Phe Trp Asn
 210 215 220
 Val Gln Leu Ser Asp His Thr Arg Ser Glu Gln Cys Tyr Arg Asp Val
 225 230 235 240
 Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys Lys Leu Arg Val
 245 250 255
 Lys Asn Lys His Val Glu Phe Phe Arg Asn Leu Tyr Leu Thr Phe Leu
 260 265 270
 Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe Gly Cys Pro Ser
 275 280 285
 Glu Ala Asp Val Asn Ser Glu Asn Leu Gln Lys Gln Leu Ser Glu Leu
 290 295 300
 Asp Glu Asp Asp Leu Cys Tyr Glu Phe Arg Arg Glu Arg Phe Thr Val
 305 310 315 320
 His Arg Thr His Leu Tyr Phe Leu His Tyr Glu Tyr Glu Pro Ala Ala
 325 330 335
 Asp Ser Thr Asp Val Thr Leu Val Ala Gln Leu Ser Met Asp Arg Leu
 340 345 350
 Gln Met Leu Glu Ala Ile Cys Lys His Trp Glu Gly Pro Ile Ser Leu
 355 360 365
 Ala Leu Tyr Leu Ser Asp Ala Glu Ala Gln Gln Phe Leu Arg Tyr Ala
 370 375 380
 Gln Gly Ser Glu Val Leu Met Ser Arg His Asn Val Gly Tyr His Ile
 385 390 395 400
 Val Tyr Lys Glu Gly Gln Phe Tyr Pro Val Asn Leu Leu Arg Asn Val
 405 410 415
 Ala Met Lys His Ile Ser Thr Pro Tyr Met Phe Leu Ser Asp Ile Asp
 420 425 430
 Phe Leu Pro Met Tyr Gly Leu Tyr Glu Tyr Leu Arg Lys Ser Val Ile
 435 440 445
 Gln Leu Asp Leu Ala Asn Thr Lys Lys Ala Met Ile Val Pro Ala Phe
 450 455 460
 Glu Thr Leu Arg Tyr Arg Leu Ser Phe Pro Lys Ser Lys Ala Glu Leu
 465 470 475 480
 Leu Ser Met Leu Asp Met Gly Thr Leu Phe Thr Phe Arg Tyr His Val
 485 490 495
 Trp Thr Lys Gly His Ala Pro Thr Asn Phe Ala Lys Trp Arg Thr Ala
 500 505 510

Thr Thr Pro Tyr Arg Val Glu Trp Glu Ala Asp Phe Glu Pro Tyr Val
 515 520 525
 Val Val Arg Arg Asp Cys Pro Glu Tyr Asp Arg Arg Phe Val Gly Phe
 530 535 540
 Gly Trp Asn Lys Val Ala His Ile Met Glu Leu Asp Val Gln Glu Tyr
 545 550 555 560
 Glu Phe Ile Val Leu Pro Asn Ala Tyr Met Ile His Met Pro His Ala
 565 570 575
 Pro Ser Phe Asp Ile Thr Lys Phe Arg Ser Asn Lys Gln Tyr Arg Ile
 580 585 590
 Cys Leu Lys Thr Leu Lys Glu Glu Phe Gln Gln Asp Met Ser Arg Arg
 595 600 605
 Tyr Gly Phe Ala Ala Leu Lys Tyr Leu Thr Ala
 610 615

<210> 49

<400> 49
000

<210> 50

<211> 230

<212> PRT

<213> *Helicobacter pylori*

<400> 50

Phe Leu Asn Leu Glu Glu Asn Asp Glu Asn Tyr Phe Tyr Gly Val Leu
 1 5 10 15
 Glu Val Glu Lys His His Met Met Glu Gly Phe Leu Phe Cys Asn Leu
 20 25 30
 Asp Tyr Gln Arg Lys Lys Asn Phe Thr Leu Arg Met His Glu Leu Leu
 35 40 45
 Arg Gly Asn Glu Ala Lys Gly Glu Leu Asp Phe Thr Lys Trp Cys Trp
 50 55 60
 Pro Asn Met Lys Ala Leu Gly Ile Glu Tyr Cys Val Phe Pro Tyr Tyr
 65 70 75 80
 Tyr Thr Ile Lys Asp Phe Ser Asn Ala Tyr Leu Asn Glu Asn Tyr Lys
 85 90 95
 Lys Thr Ile Leu Glu Ala Arg Glu Asn Pro Thr Ile Ile His Tyr Asp
 100 105 110
 Ala Trp Trp Gly Ala Val Lys Pro Trp Asp Tyr Pro Phe Gly Leu Lys
 115 120 125

Ala Asp Leu Trp Leu Asn Ala Leu Ala Lys Thr Pro Phe Met Ser Asp
130 135 140

Trp Ile Asp Ser Ile Ala Arg Val Glu Ile Gly Ser Glu Lys Trp His
145 150 155 160

Arg Tyr His Ser Ile Val Ala Tyr His Tyr Tyr Phe Pro Leu Trp Lys
165 170 175

Thr Glu Glu Gln Ile Ala His Asp Ala Leu Lys Thr Phe Leu Asp His
180 185 190

Tyr Phe Ser Cys Ile His Ala Ala Ile Lys Gln Glu Asn Leu Gly Met
195 200 205

Phe Leu Asn His Tyr Phe Ser His Ala His Ala Glu Ile Lys Glu Asn
210 215 220

Ser Leu Glu Met Phe Leu
225 230

<210> 51
<211> 756
<212> PRT
<213> Homo sapiens

<400> 51
Met Leu Gly Ile Cys Arg Gly Arg Arg Lys Phe Leu Ala Ala Ser Leu
1 5 10 15

Ser Leu Leu Cys Ile Pro Ala Ile Thr Trp Ile Tyr Leu Phe Ser Gly
20 25 30

Ser Phe Glu Asp Gly Lys Pro Val Ser Leu Ser Pro Leu Glu Ser Gln
35 40 45

Ala His Ser Pro Arg Tyr Thr Ala Ser Ser Gln Arg Glu Arg Glu Ser
50 55 60

Leu Glu Val Arg Met Arg Glu Val Glu Glu Glu Asn Arg Ala Leu Arg
65 70 75 80

Arg Gln Leu Ser Leu Ala Gln Gly Arg Ala Pro Ser His Arg Arg Gly
85 90 95

Asn His Ser Lys Thr Tyr Ser Met Glu Glu Gly Thr Gly Asp Ser Glu
100 105 110

Asn Leu Arg Ala Gly Ile Val Ala Gly Asn Ser Ser Glu Cys Gly Gln
115 120 125

Gln Pro Val Val Glu Lys Cys Glu Thr Ile His Val Ala Ile Val Cys
130 135 140

Ala Gly Tyr Asn Ala Ser Arg Asp Val Val Thr Leu Val Lys Ser Val

145		150		155		160
Leu Phe His Arg Arg Asn Pro Leu His Phe His Leu Ile Ala Asp Ser						
		165		170		175
Ile Ala Glu Gln Ile Leu Ala Thr Leu Phe Gln Thr Trp Met Val Pro						
		180		185		190
Ala Val Arg Val Asp Phe Tyr Asn Ala Asp Glu Leu Lys Ser Glu Val						
		195		200		205
Ser Trp Ile Pro Asn Lys His Tyr Ser Gly Ile Tyr Gly Leu Met Lys						
		210		215		220
Leu Val Leu Thr Lys Thr Leu Pro Ala Asn Leu Glu Arg Val Ile Val						
		225		230		235
Leu Asp Thr Asp Ile Thr Phe Ala Thr Asp Ile Ala Glu Leu Trp Ala						
		245		250		255
Val Phe His Lys Phe Lys Gly Gln Gln Val Leu Gly Leu Val Glu Asn						
		260		265		270
Gln Ser Asp Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp						
		275		280		285
Pro Ala Leu Gly His Gly Tyr Asn Thr Gly Val Ile Leu Leu Leu Leu						
		290		295		300
Asp Lys Leu Arg Lys Met Lys Trp Glu Gln Met Trp Arg Leu Thr Ala						
		305		310		315
Glu Arg Glu Leu Met Gly Met Leu Ser Thr Ser Leu Ala Asp Gln Asp						
		325		330		335
Ile Phe Asn Ala Val Ile Lys Gln Asn Pro Phe Leu Val Tyr Gln Leu						
		340		345		350
Pro Cys Phe Trp Asn Val Gln Leu Ser Asp His Thr Arg Ser Glu Gln						
		355		360		365
Cys Tyr Arg Asp Val Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro						
		370		375		380
Lys Lys Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Leu						
		385		390		395
Tyr Leu Thr Phe Leu Glu Tyr Asp Gly Asn Leu Ile Arg Arg Glu Leu						
		405		410		415
Phe Gly Cys Pro Ser Glu Ala Asp Val Asn Ser Glu Asn Leu Gln Lys						
		420		425		430
Gln Leu Ser Glu Leu Asp Glu Asp Asp Leu Cys Tyr Glu Phe Arg Arg						
		435		440		445
Glu Arg Phe Thr Val His Arg Thr His Leu Tyr Phe Leu His Tyr Glu						

450	455	460
Tyr Glu Pro Ala Ala Asp Ser Thr Asp Val Thr Leu Val Ala Gln Leu 465 470 475 480		
Ser Met Asp Arg Leu Gln Met Leu Glu Ala Ile Cys Lys His Trp Glu 485 490 495		
Gly Pro Ile Ser Leu Ala Leu Tyr Leu Ser Asp Ala Glu Ala Gln Gln 500 505 510		
Phe Leu Arg Tyr Ala Gln Gly Ser Glu Val Leu Met Ser Arg His Asn 515 520 525		
Val Gly Tyr His Ile Val Tyr Lys Glu Gly Gln Phe Tyr Pro Val Asn 530 535 540		
Leu Leu Arg Asn Val Ala Met Lys His Ile Ser Thr Pro Tyr Met Phe 545 550 555 560		
Leu Ser Asp Ile Asp Phe Leu Pro Met Tyr Gly Leu Tyr Glu Tyr Leu 565 570 575		
Arg Lys Ser Val Ile Gln Leu Asp Leu Ala Asn Thr Lys Lys Ala Met 580 585 590		
Ile Val Pro Ala Phe Glu Thr Leu Arg Tyr Arg Leu Ser Phe Pro Lys 595 600 605		
Ser Lys Ala Glu Leu Leu Ser Met Leu Asp Met Gly Thr Leu Phe Thr 610 615 620		
Phe Arg Tyr His Val Trp Thr Lys Gly His Ala Pro Thr Asn Phe Ala 625 630 635 640		
Lys Trp Arg Thr Ala Thr Thr Pro Tyr Arg Val Glu Trp Glu Ala Asp 645 650 655		
Phe Glu Pro Tyr Val Val Val Arg Arg Asp Cys Pro Glu Tyr Asp Arg 660 665 670		
Arg Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Met Glu Leu 675 680 685		
Asp Val Gln Glu Tyr Glu Phe Ile Val Leu Pro Asn Ala Tyr Met Ile 690 695 700		
His Met Pro His Ala Pro Ser Phe Asp Ile Thr Lys Phe Arg Ser Asn 705 710 715 720		
Lys Gln Tyr Arg Ile Cys Leu Lys Thr Leu Lys Glu Glu Phe Gln Gln 725 730 735		
Asp Met Ser Arg Arg Tyr Gly Phe Ala Ala Leu Lys Tyr Leu Thr Ala 740 745 750		
Glu Asn Asn Ser		

755

<210> 52
 <211> 761
 <212> PRT
 <213> Homo sapiens

<400> 52
 Ala Thr Ser Glu Arg Met Leu Gly Ile Cys Arg Gly Arg Arg Lys Phe
 1 5 10 15
 Leu Ala Ala Ser Leu Ser Leu Leu Cys Ile Pro Ala Ile Thr Trp Ile
 20 25 30
 Tyr Leu Phe Ser Gly Ser Phe Glu Asp Gly Lys Pro Val Ser Leu Ser
 35 40 45
 Pro Leu Glu Ser Gln Ala His Ser Pro Arg Tyr Thr Ala Ser Ser Gln
 50 55 60
 Arg Glu Arg Glu Ser Leu Glu Val Arg Met Arg Glu Val Glu Glu Glu
 65 70 75 80
 Asn Arg Ala Leu Arg Arg Gln Leu Ser Leu Ala Gln Gly Arg Ala Pro
 85 90 95
 Ser His Arg Arg Gly Asn His Ser Lys Thr Tyr Ser Met Glu Glu Gly
 100 105 110
 Thr Gly Asp Ser Glu Asn Leu Arg Ala Gly Ile Val Ala Gly Asn Ser
 115 120 125
 Ser Glu Cys Gly Gln Gln Pro Val Val Glu Lys Cys Glu Thr Ile His
 130 135 140
 Val Ala Ile Val Cys Ala Gly Tyr Asn Ala Ser Arg Asp Val Val Thr
 145 150 155 160
 Leu Val Lys Ser Val Leu Phe His Arg Arg Asn Pro Leu His Phe His
 165 170 175
 Leu Ile Ala Asp Ser Ile Ala Glu Gln Ile Leu Ala Thr Leu Phe Gln
 180 185 190
 Thr Trp Met Val Pro Ala Val Arg Val Asp Phe Tyr Asn Ala Asp Glu
 195 200 205
 Leu Lys Ser Glu Val Ser Trp Ile Pro Asn Lys His Tyr Ser Gly Ile
 210 215 220
 Tyr Gly Leu Met Lys Leu Val Leu Thr Lys Thr Leu Pro Ala Asn Leu
 225 230 235 240
 Glu Arg Val Ile Val Leu Asp Thr Asp Ile Thr Phe Ala Thr Asp Ile
 245 250 255

Ala Glu Leu Trp Ala Val Phe His Lys Phe Lys Gly Gln Gln Val Leu
 260 265 270
 Gly Leu Val Glu Asn Gln Ser Asp Trp Tyr Leu Gly Asn Leu Trp Lys
 275 280 285
 Asn His Arg Pro Trp Pro Ala Leu Gly Arg Gly Tyr Asn Thr Gly Val
 290 295 300
 Ile Leu Leu Leu Leu Asp Lys Leu Arg Lys Met Lys Trp Glu Gln Met
 305 310 315 320
 Trp Arg Leu Thr Ala Glu Arg Glu Leu Met Gly Met Leu Ser Thr Ser
 325 330 335
 Leu Ala Asp Gln Asp Ile Phe Asn Ala Val Ile Lys Gln Asn Pro Phe
 340 345 350
 Leu Val Tyr Gln Leu Pro Cys Phe Trp Asn Val Gln Leu Ser Asp His
 355 360 365
 Thr Arg Ser Glu Gln Cys Tyr Arg Asp Val Ser Asp Leu Lys Val Ile
 370 375 380
 His Trp Asn Ser Pro Lys Lys Leu Arg Val Lys Asn Lys His Val Glu
 385 390 395 400
 Phe Phe Arg Asn Leu Tyr Leu Thr Phe Leu Glu Tyr Asp Gly Asn Leu
 405 410 415
 Ile Arg Arg Glu Leu Phe Gly Cys Pro Ser Glu Ala Asp Val Asn Ser
 420 425 430
 Glu Asn Leu Gln Lys Gln Leu Ser Glu Leu Asp Glu Asp Asp Leu Cys
 435 440 445
 Tyr Glu Phe Arg Arg Glu Arg Phe Thr Val His Arg Thr His Leu Tyr
 450 455 460
 Phe Leu His Tyr Glu Tyr Glu Pro Ala Ala Asp Ser Thr Asp Val Thr
 465 470 475 480
 Leu Val Ala Gln Leu Ser Met Asp Arg Leu Gln Met Leu Glu Ala Ile
 485 490 495
 Cys Lys His Trp Glu Gly Pro Ile Ser Leu Ala Leu Tyr Leu Ser Asp
 500 505 510
 Ala Glu Ala Gln Gln Phe Leu Arg Tyr Ala Gln Gly Ser Glu Val Leu
 515 520 525
 Met Ser Arg His Asn Val Gly Tyr His Ile Val Tyr Lys Glu Gly Gln
 530 535 540
 Phe Tyr Pro Val Asn Leu Leu Arg Asn Val Ala Met Lys His Ile Ser
 545 550 555 560

Thr Pro Tyr Met Phe Leu Ser Asp Ile Asp Phe Leu Pro Met Tyr Gly
 565 570 575
 Leu Val Glu Tyr Leu Arg Lys Ser Val Ile Gln Leu Asp Leu Ala Asn
 580 585 590
 Thr Lys Lys Ala Met Ile Val Pro Ala Phe Glu Thr Leu Arg Tyr Arg
 595 600 605
 Leu Ser Phe Pro Lys Ser Lys Ala Glu Leu Leu Ser Met Leu Asp Met
 610 615 620
 Gly Thr Leu Phe Thr Phe Arg Tyr His Val Trp Thr Lys Gly His Ala
 625 630 635 640
 Pro Thr Asn Phe Ala Lys Trp Arg Thr Ala Thr Thr Pro Tyr Arg Val
 645 650 655
 Glu Trp Glu Ala Asp Phe Glu Pro Tyr Val Val Val Arg Arg Asp Cys
 660 665 670
 Pro Glu Tyr Asp Arg Arg Phe Val Gly Phe Gly Trp Asn Lys Val Ala
 675 680 685
 His Ile Met Glu Leu Asp Val Gln Glu Tyr Glu Phe Ile Val Leu Pro
 690 695 700
 Asn Ala Tyr Met Ile His Met Pro His Ala Pro Ser Phe Asp Ile Thr
 705 710 715 720
 Lys Phe Arg Ser Asn Lys Gln Tyr Arg Ile Cys Leu Lys Thr Leu Lys
 725 730 735
 Glu Glu Phe Gln Gln Asp Met Ser Arg Arg Tyr Gly Phe Ala Ala Leu
 740 745 750
 Lys Tyr Leu Thr Ala Glu Asn Asn Ser
 755 760

<210> 53
 <211> 756
 <212> PRT
 <213> Mus musculus

<400> 53
 Met Leu Gly Ile Cys Arg Gly Arg Arg Lys Phe Leu Ala Ala Ser Leu
 1 5 10 15
 Thr Leu Leu Cys Ile Pro Ala Ile Thr Trp Ile Tyr Leu Phe Ala Gly
 20 25 30
 Ser Phe Glu Asp Gly Lys Pro Val Ser Leu Ser Pro Leu Glu Ser Gln
 35 40 45
 Ala His Ser Pro Arg Tyr Thr Ala Ser Ser Gln Arg Glu Arg Glu Ser
 50 55 60

Leu Glu Val Arg Val Arg Glu Val Glu Glu Glu Asn Arg Ala Leu Arg
 65 70 75 80
 Arg Gln Leu Ser Leu Ala Gln Gly Gln Ser Pro Ala His His Arg Gly
 85 90 95
 Asn His Ser Lys Thr Tyr Ser Met Glu Glu Gly Thr Gly Asp Ser Glu
 100 105 110
 Asn Leu Arg Ala Gly Ile Val Ala Gly Asn Ser Ser Glu Cys Gly Gln
 115 120 125
 Gln Pro Ala Val Glu Lys Cys Glu Thr Ile His Val Ala Ile Val Cys
 130 135 140
 Ala Gly Tyr Asn Ala Ser Arg Asp Val Val Thr Leu Val Lys Ser Val
 145 150 155 160
 Leu Phe His Arg Arg Asn Pro Leu His Phe His Leu Ile Ala Asp Ser
 165 170 175
 Ile Ala Glu Gln Ile Leu Ala Thr Leu Phe Gln Thr Trp Met Val Pro
 180 185 190
 Ala Val Arg Val Asp Phe Tyr Asn Ala Asp Glu Leu Lys Ser Glu Val
 195 200 205
 Ser Trp Ile Pro Asn Lys His Tyr Ser Gly Ile Tyr Gly Leu Met Lys
 210 215 220
 Leu Val Leu Thr Lys Thr Leu Pro Ala Asn Leu Glu Arg Val Ile Val
 225 230 235 240
 Leu Asp Thr Asp Ile Thr Phe Ala Thr Asp Ile Ala Glu Leu Trp Ala
 245 250 255
 Val Phe His Lys Phe Lys Gly Gln Gln Val Leu Gly Leu Val Glu Asn
 260 265 270
 Gln Ser Asp Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp
 275 280 285
 Pro Ala Leu Gly Arg Gly Tyr Asn Thr Gly Val Ile Leu Leu Leu Leu
 290 295 300
 Asp Lys Leu Arg Lys Met Lys Trp Glu Gln Met Trp Arg Leu Thr Ala
 305 310 315 320
 Glu Arg Glu Leu Met Gly Met Leu Ser Thr Ser Leu Ala Asp Gln Asp
 325 330 335
 Ile Phe Asn Ala Val Ile Lys Gln Asn Pro Phe Leu Val Tyr Gln Leu
 340 345 350
 Pro Cys Phe Trp Asn Val Gln Leu Ser Asp His Thr Arg Ser Glu Gln
 355 360 365

Cys	Tyr	Arg	Asp	Val	Ser	Asp	Leu	Lys	Val	Ile	His	Trp	Asn	Ser	Pro	370	375	380	
Lys	Lys	Leu	Arg	Val	Lys	Asn	Lys	His	Val	Glu	Phe	Phe	Arg	Asn	Leu	385	390	395	400
Tyr	Leu	Thr	Phe	Leu	Glu	Tyr	Asp	Gly	Asn	Leu	Ile	Arg	Arg	Glu	Leu	405	410	415	
Phe	Gly	Cys	Pro	Ser	Glu	Thr	Asp	Val	Asn	Asn	Glu	Asn	Leu	Gln	Lys	420	425	430	
Gln	Leu	Ser	Glu	Leu	Asp	Glu	Asp	Asp	Leu	Cys	Tyr	Glu	Phe	Arg	Arg	435	440	445	
Glu	Arg	Phe	Thr	Val	His	Arg	Thr	His	Leu	Tyr	Phe	Leu	His	Tyr	Glu	450	455	460	
Phe	Glu	Pro	Ser	Ala	Asp	Asn	Thr	Asp	Val	Thr	Leu	Val	Ala	Gln	Leu	465	470	475	480
Ser	Met	Asp	Arg	Leu	Gln	Met	Leu	Glu	Ala	Ile	Cys	Lys	His	Trp	Glu	485	490	495	
Gly	Pro	Ile	Ser	Leu	Ala	Leu	Tyr	Leu	Ser	Asp	Ala	Glu	Ala	Gln	Gln	500	505	510	
Phe	Leu	Arg	Tyr	Ala	Gln	Gly	Ser	Glu	Val	Leu	Met	Ser	Arg	Gln	Asn	515	520	525	
Val	Gly	Tyr	His	Ile	Val	Tyr	Lys	Glu	Gly	Gln	Phe	Tyr	Pro	Val	Asn	530	535	540	
Leu	Leu	Arg	Asn	Val	Ala	Met	Lys	His	Ile	Ser	Thr	Pro	Tyr	Met	Phe	545	550	555	560
Leu	Ser	Asp	Ile	Asp	Phe	Leu	Pro	Met	Tyr	Gly	Leu	Val	Glu	Tyr	Leu	565	570	575	
Arg	Lys	Ser	Val	Ile	Gln	Leu	Asp	Leu	Ala	Asn	Thr	Lys	Lys	Ala	Met	580	585	590	
Ile	Val	Pro	Ala	Phe	Glu	Thr	Leu	Arg	Tyr	Arg	Leu	Ser	Phe	Pro	Lys	595	600	605	
Ser	Lys	Ala	Glu	Leu	Leu	Ser	Met	Leu	Asp	Met	Gly	Thr	Leu	Phe	Thr	610	615	620	
Phe	Arg	Tyr	His	Val	Trp	Thr	Lys	Gly	His	Ala	Pro	Thr	Asn	Phe	Ala	625	630	635	640
Lys	Trp	Arg	Thr	Ala	Thr	Thr	Pro	Tyr	Gln	Val	Glu	Trp	Glu	Ala	Asp	645	650	655	
Phe	Glu	Pro	Tyr	Val	Val	Val	Arg	Arg	Asp	Cys	Pro	Glu	Tyr	Asp	Arg	660	665	670	

Arg Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Met Glu Leu
675 680 685

Asp Ala Gln Glu Tyr Glu Phe Thr Val Leu Pro Asn Ala Tyr Met Ile
690 695 700

His Met Pro His Ala Pro Ser Phe Asp Ile Thr Lys Phe Arg Ser Asn
705 710 715 720

Lys Gln Tyr Arg Ile Cys Leu Lys Thr Leu Lys Glu Glu Phe Gln Gln
725 730 735

Asp Met Ser Arg Arg Tyr Gly Phe Ala Ala Leu Lys Tyr Leu Thr Ala
740 745 750

Glu Asn Asn Ser
755

<210> 54
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:chemically
synthesized

<400> 54
tggagaacca gagtgactgg ta 22

<210> 55
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:chemically
synthesized

<400> 55
aacctctgga agaaccacag gccct 25

<210> 56
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:chemically
synthesized

<400> 56
agcaggatca cacctgtggt aa 22

<210> 57
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:chemically
 synthesized

 <400> 57
 ggatccgagg actctggttg gtgtgggcct gtgtgc 36

 <210> 58
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:chemically
 synthesized

 <400> 58
 ctcgaggaca tcttgcaaac cctgtgctgt gatgg 35

 <210> 59
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:chemically
 synthesized

 <400> 59
 agatctcggg aggctgcgga gagccgccgc cctcgacg 38

 <210> 60
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:chemically
 synthesized

 <400> 60
 ctcgaggcct cgggcagggc tctggggctg ctgcagg 37

 <210> 61
 <211> 20
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:chemically synthesized
 <400> 61
 cacttggtga ctgacgccgt 20
 <210> 62
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:chemically synthesized
 <400> 62
 acggcgtcag tcaccaagtg 20
 <210> 63
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:chemically synthesized
 <400> 63
 cggcaggctg gctgggagc 19
 <210> 64
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:chemically synthesized
 <400> 64
 gctcccagcc agcctgccg 19
 <210> 65
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:chemically synthesized

<400> 65
 gctgcggaga gagctctt 18

<210> 66
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:chemically
 synthesized

<400> 66
 aagagctctc tccgcagc 18

<210> 67
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:chemically
 synthesized

<400> 67
 cgaggcctca ccagtgttg c 21

<210> 68
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:chemically
 synthesized

<400> 68
 gcaagcactg gtgaggcctc g 21

<210> 69
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:chemically
 synthesized

<400> 69
 gcactctcta caccttcag 19

<210> 70
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:chemically synthesized

<400> 70
 ctgaaggtgt agagagtgc 19

<210> 71
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:chemically synthesized

<400> 71
 agatctaacc gctccgactg cggccccgcag c 31

<210> 72
 <211> 1926
 <212> DNA
 <213> Homo sapiens

<400> 72
 aaccgctccg actgcgggccc gcagccgccc cgcgcccca agtgcgagct cttgcatgtg 60
 gccatcgtgt gtgcggggca taactccagc cgagacgtca tcaccctggg gaagtccatg 120
 ctcttctaca ggaaaaatcc actgcacctc cacttggtga ctgacgccgt ggccagaaac 180
 atcctggaga cgctcttcca cacatggatg gtgcctgctg tccgtgtcag cttttatcat 240
 accgaccagc tcaagcccca ggtctcctgg atccccaaca agcactactc cggcctctat 300
 gggctaataa agctgggtgct gcccagtgcc ttgcctgctg agctggcccg cgtcattgtc 360
 ctggacacgg atgtcacctt cgctctgac atctcggagc tctgggccct ctgtgctcac 420
 ttttctgaca cgcaggcgat cggctctgtg gagaaccaga gtgactggta cctgggcaac 480
 ctctggaaga accacaggcc ctggcctgcc ttgggcccgg gatttaacac aggtgtgatc 540
 ctgctgcggc tggaccggct ccggcaggct ggctgggagc agatgtggag gctgacagcc 600
 aggcgggagc tccttagcct gcctgccacc tcaactggctg accaggacat cttcaacgct 660
 gtgatcaagg agcaccgggg gctagtgcag cgtctgcctt gtgtctggaa tgtgcagctg 720
 tcagatcaca cactggccga gcgctgctac tctgaggcgt ctgacctcaa ggtgatccac 780
 tggaaactac caaagaagct tcgggtgaag aacaagcatg tgggaattctt ccgcaatttc 840
 tacctgacct tcctggagta cgatgggaac ctgctgcgga gagagctctt tgtgtgcccc 900
 agccagcccc cacctgggtgc tgagcagttg cagcaggccc tggcacaact ggacgaggaa 960
 gacccctgct ttgagttccg gcagcagcag ctcactgtgc accgtgtgca tgtcactttc 1020
 ctgccccatg aaccgccacc cccccggcct cactagtcca cccttggtgg ccagctgtcc 1080
 atggaccggc tgcagatggt ggaagccctg tgcaggcact ggcctggccc catgagcctg 1140
 gccttgtacc tgacagacgc agaagctcag cagttcctgc atttcgtcga ggcctcacca 1200
 gtgcttgtct cccggcagga cgtggcctac catgtggtgt accgtgaggg gccctatac 1260
 cccgtcaacc agcttcgcaa cgtggccttg gccaggccc tcacgcctta cgtcttcttc 1320
 agtgacattg acttctctgc tgctattctt ctctacgact acctcagggc ctccattgag 1380
 cagctggggc tgggcagccg gcgcaaggca gcactggtgg tgccggcatt tgagaccctg 1440
 cgctaccgct tcagcttccc ccattccaag gtggagctgt tggccttgct ggatgcgggc 1500

actctctaca ccttcaggta ccacgagtgg ccccgaggcc acgcacccac agactatgcc 1560
cgctggcggg aggtcaggc cccgtaccgt gtgcaatggg cggccaacta tgaaccctac 1620
gtggtggtgc cagcagactg tccccgctat gatcctcgct ttgtgggctt cggctggaac 1680
aaagtggccc acattgtgga gctggatgcc caggaatatg agctcctggt gctgcccag 1740
gccttcacca tccatctgcc ccacgtcca agcctggaca tctcccgtt cgcctccagc 1800
cccacctatc gtgactgcct ccaggccctc aaggacgaat tccaccagga cttgtcccgc 1860
caccatgggg ctgctgccct caaatacctc ccagccctgc agcagcccca gagccctgcc 1920
cgaggc 1926

<210> 73
<211> 642
<212> PRT
<213> Homo sapiens

<400> 73
Asn Arg Ser Asp Cys Gly Pro Gln Pro Pro Pro Pro Pro Lys Cys Glu
1 5 10 15
Leu Leu His Val Ala Ile Val Cys Ala Gly His Asn Ser Ser Arg Asp
20 25 30
Val Ile Thr Leu Val Lys Ser Met Leu Phe Tyr Arg Lys Asn Pro Leu
35 40 45
His Leu His Leu Val Thr Asp Ala Val Ala Arg Asn Ile Leu Glu Thr
50 55 60
Leu Phe His Thr Trp Met Val Pro Ala Val Arg Val Ser Phe Tyr His
65 70 75 80
Thr Asp Gln Leu Lys Pro Gln Val Ser Trp Ile Pro Asn Lys His Tyr
85 90 95
Ser Gly Leu Tyr Gly Leu Met Lys Leu Val Leu Pro Ser Ala Leu Pro
100 105 110
Ala Glu Leu Ala Arg Val Ile Val Leu Asp Thr Asp Val Thr Phe Ala
115 120 125
Ser Asp Ile Ser Glu Leu Trp Ala Leu Cys Ala His Phe Ser Asp Thr
130 135 140
Gln Ala Ile Gly Leu Val Glu Asn Gln Ser Asp Trp Tyr Leu Gly Asn
145 150 155 160
Leu Trp Lys Asn His Arg Pro Trp Pro Ala Leu Gly Arg Gly Phe Asn
165 170 175
Thr Gly Val Ile Leu Leu Arg Leu Asp Arg Leu Arg Gln Ala Gly Trp
180 185 190
Glu Gln Met Trp Arg Leu Thr Ala Arg Arg Glu Leu Leu Ser Leu Pro
195 200 205
Ala Thr Ser Leu Ala Asp Gln Asp Ile Phe Asn Ala Val Ile Lys Glu
210 215 220

His Pro Gly Leu Val Gln Arg Leu Pro Cys Val Trp Asn Val Gln Leu
 225 230 235 240
 Ser Asp His Thr Leu Ala Glu Arg Cys Tyr Ser Glu Ala Ser Asp Leu
 245 250 255
 Lys Val Ile His Trp Asn Ser Pro Lys Lys Leu Arg Val Lys Asn Lys
 260 265 270
 His Val Glu Phe Phe Arg Asn Phe Tyr Leu Thr Phe Leu Glu Tyr Asp
 275 280 285
 Gly Asn Leu Leu Arg Arg Glu Leu Phe Val Cys Pro Ser Gln Pro Pro
 290 295 300
 Pro Gly Ala Glu Gln Leu Gln Gln Ala Leu Ala Gln Leu Asp Glu Glu
 305 310 315 320
 Asp Pro Cys Phe Glu Phe Arg Gln Gln Gln Leu Thr Val His Arg Val
 325 330 335
 His Val Thr Phe Leu Pro His Glu Pro Pro Pro Pro Arg Pro His Asp
 340 345 350
 Val Thr Leu Val Ala Gln Leu Ser Met Asp Arg Leu Gln Met Leu Glu
 355 360 365
 Ala Leu Cys Arg His Trp Pro Gly Pro Met Ser Leu Ala Leu Tyr Leu
 370 375 380
 Thr Asp Ala Glu Ala Gln Gln Phe Leu His Phe Val Glu Ala Ser Pro
 385 390 395 400
 Val Leu Ala Ala Arg Gln Asp Val Ala Tyr His Val Val Tyr Arg Glu
 405 410 415
 Gly Pro Leu Tyr Pro Val Asn Gln Leu Arg Asn Val Ala Leu Ala Gln
 420 425 430
 Ala Leu Thr Pro Tyr Val Phe Leu Ser Asp Ile Asp Phe Leu Pro Ala
 435 440 445
 Tyr Ser Leu Tyr Asp Tyr Leu Arg Ala Ser Ile Glu Gln Leu Gly Leu
 450 455 460
 Gly Ser Arg Arg Lys Ala Ala Leu Val Val Pro Ala Phe Glu Thr Leu
 465 470 475 480
 Arg Tyr Arg Phe Ser Phe Pro His Ser Lys Val Glu Leu Leu Ala Leu
 485 490 495
 Leu Asp Ala Gly Thr Leu Tyr Thr Phe Arg Tyr His Glu Trp Pro Arg
 500 505 510
 Gly His Ala Pro Thr Asp Tyr Ala Arg Trp Arg Glu Ala Gln Ala Pro
 515 520 525

Tyr Arg Val Gln Trp Ala Ala Asn Tyr Glu Pro Tyr Val Val Val Pro
 530 535 540
 Arg Asp Cys Pro Arg Tyr Asp Pro Arg Phe Val Gly Phe Gly Trp Asn
 545 550 555 560
 Lys Val Ala His Ile Val Glu Leu Asp Ala Gln Glu Tyr Glu Leu Leu
 565 570 575
 Val Leu Pro Glu Ala Phe Thr Ile His Leu Pro His Ala Pro Ser Leu
 580 585 590
 Asp Ile Ser Arg Phe Arg Ser Ser Pro Thr Tyr Arg Asp Cys Leu Gln
 595 600 605
 Ala Leu Lys Asp Glu Phe His Gln Asp Leu Ser Arg His His Gly Ala
 610 615 620
 Ala Ala Leu Lys Tyr Leu Pro Ala Leu Gln Gln Pro Gln Ser Pro Ala
 625 630 635 640
 Arg Gly

<210> 74
 <211> 695
 <212> PRT
 <213> Homo sapiens

<400> 74
 Met Leu Pro Arg Gly Arg Pro Arg Ala Leu Gly Ala Ala Ala Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Gly Phe Leu Leu Phe Gly Gly Asp Leu Gly
 20 25 30
 Arg Glu Ala Ala Glu Ser Arg Arg Pro Arg Arg Asn Pro Gly Gly Pro
 35 40 45
 Ala Pro Gly Thr Thr Thr Ala Pro Thr Ala Ala Arg Ser Arg Arg Arg
 50 55 60
 Pro Pro Lys Cys Glu Leu Leu His Val Ala Ile Val Cys Ala Gly His
 65 70 75 80
 Asn Ser Ser Arg Asp Val Ile Ile Leu Val Lys Ser Met Leu Phe Tyr
 85 90 95
 Arg Lys Asn Pro Leu His Leu His Leu Val Thr Asp Ala Val Ala Arg
 100 105 110
 Asn Ile Leu Glu Thr Leu Phe His Thr Trp Met Val Pro Ala Val Arg
 115 120 125
 Val Ser Phe Tyr His Ala Asp Gln Leu Lys Pro Gln Val Ser Trp Ile

130	135	140
Pro Asn Lys His Tyr Ser Gly Leu Tyr Gly Leu Met Lys Leu Val Leu 145 150 155 160		
Pro Ser Ala Leu Pro Ala Glu Leu Ala Arg Val Ile Val Leu Asp Thr 165 170 175		
Asp Val Thr Phe Ala Ser Asp Ile Ser Glu Leu Trp Ala Leu Phe Ala 180 185 190		
His Phe Ser Asp Thr Gln Ala Ile Gly Leu Val Glu Asn Gln Ser Asp 195 200 205		
Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro Ala Leu 210 215 220		
Gly Arg Gly Phe Asn Thr Gly Val Ile Leu Leu Arg Leu Asp Arg Leu 225 230 235 240		
Arg Gln Ala Gly Trp Glu Gln Met Trp Arg Leu Thr Ala Arg Arg Glu 245 250 255		
Leu Leu Ser Leu Pro Ala Thr Ser Leu Ala Asp Gln Asp Ile Phe Asn 260 265 270		
Ala Val Ile Lys Glu His Pro Gly Leu Val Gln Arg Leu Pro Cys Val 275 280 285		
Trp Asn Val Gln Leu Ser Asp His Thr Leu Ala Glu Arg Cys Tyr Ser 290 295 300		
Glu Ala Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys Lys Leu 305 310 315 320		
Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Phe Tyr Leu Thr 325 330 335		
Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe Val Cys 340 345 350		
Pro Ser Gln Pro Pro Pro Gly Ala Glu Gln Leu Gln Gln Ala Leu Ala 355 360 365		
Gln Leu Asp Glu Glu Asp Pro Cys Phe Glu Phe Arg Gln Gln Gln Leu 370 375 380		
Thr Val His Arg Val His Val Thr Phe Leu Pro His Glu Pro Pro Pro 385 390 395 400		
Pro Arg Pro His Asp Val Thr Leu Val Ala Gln Leu Ser Met Asp Arg 405 410 415		
Leu Gln Met Leu Glu Ala Leu Cys Arg His Trp Pro Gly Pro Met Ser 420 425 430		
Leu Ala Leu Tyr Leu Thr Asp Ala Glu Ala Gln Gln Phe Leu His Phe		

435				440				445							
Val	Glu	Ala	Ser	Pro	Val	Leu	Ala	Ala	Arg	Gln	Asp	Val	Ala	Tyr	His
450						455					460				
Val	Val	Tyr	Arg	Glu	Gly	Pro	Leu	Tyr	Pro	Val	Asn	Gln	Leu	Arg	Asn
465					470					475					480
Val	Ala	Leu	Ala	Gln	Ala	Leu	Thr	Pro	Tyr	Val	Phe	Leu	Ser	Asp	Ile
				485					490					495	
Asp	Phe	Leu	Pro	Ala	Tyr	Ser	Leu	Tyr	Asp	Tyr	Leu	Arg	Ala	Ser	Ile
			500						505				510		
Glu	Gln	Leu	Gly	Leu	Gly	Ser	Arg	Arg	Lys	Ala	Ala	Leu	Val	Val	Pro
		515					520						525		
Ala	Phe	Glu	Thr	Leu	Arg	Tyr	Arg	Phe	Ser	Phe	Pro	His	Ser	Lys	Val
	530					535					540				
Glu	Leu	Leu	Ala	Leu	Leu	Asp	Ala	Gly	Thr	Leu	Tyr	Thr	Phe	Arg	Tyr
545					550					555					560
His	Glu	Trp	Pro	Arg	Gly	His	Ala	Pro	Thr	Asp	Tyr	Ala	Arg	Trp	Arg
				565					570					575	
Glu	Ala	Gln	Ala	Pro	Tyr	Arg	Val	Gln	Trp	Ala	Ala	Asn	Tyr	Glu	Pro
			580						585				590		
Tyr	Val	Val	Val	Pro	Arg	Asp	Cys	Pro	Arg	Tyr	Asp	Pro	Arg	Phe	Val
	595						600					605			
Gly	Phe	Gly	Trp	Asn	Lys	Val	Ala	His	Ile	Val	Glu	Leu	Asp	Ala	Gln
	610					615					620				
Glu	Tyr	Glu	Leu	Leu	Val	Leu	Pro	Glu	Ala	Phe	Thr	Ile	His	Leu	Pro
625					630					635					640
His	Ala	Pro	Ser	Leu	Asp	Ile	Ser	Arg	Phe	Arg	Ser	Ser	Pro	Thr	Tyr
				645					650					655	
Arg	Asp	Cys	Leu	Gln	Ala	Leu	Lys	Asp	Glu	Phe	His	Gln	Asp	Leu	Ser
			660						665				670		
Arg	His	His	Gly	Ala	Ala	Ala	Leu	Lys	Tyr	Leu	Pro	Ala	Leu	Gln	Gln
	675						680						685		
Pro	Gln	Ser	Pro	Ala	Arg	Gly									
	690					695									

<210> 75
 <211> 617
 <212> PRT
 <213> Homo sapiens
 <220>

<221> VARIANT

<222> (50)

<223> where Xaa is any amino acid as defined in the
specification

<400> 75

Met Leu Leu Leu Leu Gly Pro Leu Arg Leu Pro Leu Cys Pro Pro Lys
1 5 10 15

Arg Lys Asn Pro Leu His Leu His Leu Val Thr Asp Ala Val Ala Arg
20 25 30

Asn Ile Leu Glu Thr Leu Phe His Thr Trp Met Val Pro Ala Ile Asp
35 40 45

Pro Xaa Val Ser Phe Tyr His Ala Asp Gln Leu Lys Pro Gln Val Ser
50 55 60

Trp Ile Pro Asn Lys His Tyr Ser Gly Leu Tyr Gly Leu Met Lys Leu
65 70 75 80

Val Leu Pro Asn Ala Leu Pro Ala Glu Leu Ala Arg Val Ile Val Leu
85 90 95

Asp Thr Asp Val Thr Phe Ala Ser Asp Ile Ser Glu Leu Trp Ala Leu
100 105 110

Cys Ala His Phe Ser Asp Thr Gln Ala Ile Gly Leu Val Glu Asn Gln
115 120 125

Ser Asp Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro
130 135 140

Ala Leu Gly Arg Gly Phe Asn Thr Gly Val Ile Leu Leu Arg Leu Asp
145 150 155 160

Arg Leu Arg Gln Ala Gly Trp Glu Gln Met Trp Arg Leu Thr Ala Arg
165 170 175

Arg Glu Leu Leu Ser Leu Pro Ala Thr Ser Leu Ala Asp Gln Asp Ile
180 185 190

Phe Asn Ala Val Ile Lys Glu His Pro Gly Leu Val Gln Arg Leu Pro
195 200 205

Cys Val Trp Asn Val Gln Leu Ser Asp His Thr Leu Ala Glu Arg Cys
210 215 220

Tyr Ser Glu Ala Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys
225 230 235 240

Lys Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Phe Tyr
245 250 255

Leu Thr Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe
260 265 270

Val Cys Pro Ser Gln Pro Pro Pro Gly Ala Glu Gln Leu Gln Gln Ala
275 280 285
Leu Ala Gln Leu Asp Glu Glu Asp Pro Cys Phe Glu Phe Arg Gln Gln
290 295 300
Gln Leu Thr Val His Arg Val His Val Thr Phe Leu Pro His Glu Pro
305 310 315 320
Pro Pro Pro Arg Pro His Asp Val Thr Leu Val Ala Gln Leu Ser Met
325 330 335
Asp Arg Leu Gln Met Leu Glu Ala Leu Cys Arg His Trp Pro Gly Pro
340 345 350
Met Ser Leu Ala Leu Tyr Leu Thr Asp Ala Glu Ala Gln Gln Phe Leu
355 360 365
His Phe Val Glu Ala Ser Pro Val Leu Ala Ala Arg Gln Asp Val Ala
370 375 380
Tyr His Val Val Tyr Arg Glu Gly Pro Leu Tyr Pro Val Asn Gln Leu
385 390 395 400
Arg Asn Val Ala Leu Ala Gln Ala Leu Thr Pro Tyr Val Phe Leu Ser
405 410 415
Asp Ile Asp Phe Leu Pro Ala Tyr Ser Leu Tyr Asp Tyr Leu Arg Ala
420 425 430
Ser Ile Glu Gln Leu Gly Leu Gly Ser Arg Arg Lys Ala Ala Leu Val
435 440 445
Val Pro Ala Phe Glu Thr Leu Arg Tyr Arg Phe Ser Phe Pro His Ser
450 455 460
Lys Val Glu Leu Leu Ala Leu Leu Asp Ala Gly Thr Leu Tyr Thr Phe
465 470 475 480
Arg Tyr His Glu Trp Pro Arg Gly His Ala Pro Thr Asp Tyr Ala Arg
485 490 495
Trp Arg Glu Ala Gln Ala Pro Tyr Arg Val Gln Trp Ala Ala Asn Tyr
500 505 510
Glu Pro Tyr Val Val Val Pro Arg Asp Cys Pro Arg Tyr Asp Pro Arg
515 520 525
Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Val Glu Leu Asp
530 535 540
Ala Gln Glu Tyr Glu Leu Leu Val Leu Pro Glu Ala Phe Thr Ile His
545 550 555 560
Leu Pro His Ala Pro Ser Leu Asp Ile Ser Arg Phe Arg Ser Ser Pro
565 570 575



C23
cont

Thr	Tyr	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Lys	Asp	Glu	Phe	His	Gln	Asp
			580					585					590		
Leu	Ser	Arg	His	His	Gly	Ala	Ala	Ala	Leu	Lys	Tyr	Leu	Pro	Ala	Leu
			595					600					605		
Gln	Gln	Pro	Gln	Ser	Pro	Ala	Arg	Gly							
			610					615							
